## REMARKS

Upon entry of the foregoing amendments, allowed claims 33, 34 and 49-52, 54, 55 and 57-60, amended claim 61, and new claim 62 will be pending. Claims 33, 59, 60, 61 and 62 are the only pending independent claims.

This Amendment After Final Rejection is filed to provide two more claims to the several already allowed claims in the belief that amended claim 61 and new claim 62 will result in complete allowance of all pending claims in this application.

**Explanation of and Support for the Amended and New Claims**

Claim 61 has been amended to include the term "wherein the isolated protein is not a wild-type NhhA polypeptide." This is supported at least by the following locations of the application as filed:

Page 3, lines 1-7 read as follows (emphasis added):

> In a first aspect, the invention provides an isolated protein comprising twelve or more contiguous conserved amino acids sequences of an NhhA polypeptide, said isolated protein excluding wild-type NhhA polypeptides.
>
> Suitably, the protein of the invention is capable of eliciting an immune response.
>
> Preferably, the immune response is less strain-specific than that elicited by said corresponding wild-type NhhA polypeptide.

Page 3, lines 18-21 state (emphasis added):

> It will be appreciated that according to this aspect, suitably one or more non-conserved amino acids of a variable region of an NhhA polypeptide, designated as V1, V2, V3 or V4 regions in FIG. 1, are deleted with respect to a wild-type NhhA polypeptide.

Additionally, page 4, lines 14-15 provide (emphasis added):

> Specifically excluded from the scope of the invention are wild-type NhhA polypeptides and *nhhA* nucleic acids.

Thus, it should be beyond question that the amendment to claim 61 is fully supported by the application as filed and its entry is respectfully requested.

New claim 62 has the same preamble and final clause as claim 61, but recites that "the isolated protein is a deletion mutant of a wild-type NhhA polypeptide." This is supported in the application as filed at least at the following locations:

Page 8, lines 3-5 read (emphasis added):

> FIG. 5: (A) Amino acid sequence of PMC 21 NhhA deletion mutant polypeptide (SEQ ID NO: 23) produced in Example 4; and (B) encoding nucleotide sequence (SEQ ID NO: 28).

Page 10, lines 8-11 state (emphasis added):

> FIG. 14: Predicted mature NhhA polypeptide deletion mutants. A: predicted mature protein described in Example 2 (SEQ ID NO:33); B: predicted mature protein described in Example 3 (SEQ ID NO:34); C: predicted mature protein described in Example 4 (SEQ ID NO:35); ....

Furthermore, at page 11, lines 21-24, the term "deletion mutant" is defined as polypeptdes where at least one of V1, V2, V3 or V4 have been deleted.

It is clear that the quoted portions, as well as the referenced Figs. and Example 4 clearly support claim 62, and therefore, its entry is respectfully requested.

**Response to Anticipation Rejections**

Claim 61 was the only claim rejected in the outstanding Office Action. It was rejected under 35 U.S.C. § 102(a) on the grounds that it was anticipated by Masignani et al. WO 99/36544 ("Masignani"). The Examiner took the position that Masignani teaches (Abstract and pages 29-30) proteins from *Neisseria meningitidis* immunogenic compositions as well as pharmaceutical compositions containing the polypeptide of claim 61, and further that Masignani teaches (page 20) a fusion protein that can provide an alternative to direct protein expression, and that Masignani's *N. meningitidis* protein ORF40-1 (SEQ ID NO:4) has an amino acid sequence of 98.1% identity to Applicants' SEQ ID NO:23 and that has 99.3% identity to Applicants' SEQ ID NO:35.

Claim 61 also was rejected under 35 U.S.C. § 102(a) on the grounds that it was anticipated by Peak et al WO 99/31132 ("Peak '132"). The Peak of this reference is the same person as the first named Applicant Peak in the present application. The Examiner took the position that Peak 132 teaches (Abstract and pages 34-40) *N. meningitidis* proteins and pharmaceutical compositions containing the polypeptide of claim 61, and further that Peak 132

teaches an *N. meningitidis* protein (SEQ ID NO:21) having an amino acid sequence of 98.1% identity to Applicants' SEQ ID NO:23 and that has 99.3% identity to Applicants' SEQ ID NO:35.

Claim 61 also was rejected under 35 U.S.C. § 102(e) on the grounds that it was anticipated by Peak et al. U.S. Patent 6,197,312 ("Peak '312") for the identical reasons as stated regarding the anticipation rejection over Peak 312. In fact, Peak 312 is the U.S. patent that issued based on the national phase of Peak 132, and thereby has the same disclosure as Peak 132. As a result, both Peak 132 and Peak '312 will be referred to together merely as "Peak."

Applicants respectfully traverse these anticipation rejections.

Initially, as reported in the Amendment After Final Rejection filed December 11, 2006 (the "Prior Amendment"), a ClustalW comparison (submitted with the Prior Amendment) of SEQ ID NO:23 with SEQ ID NO:4 of Masignani reveals only about 86% identity over the entire, wild-type sequences; a ClustalW comparison (submitted with the Prior Amendment) of SEQ ID NO:35 with SEQ ID NO:4 of Masignani reveals only 77% identity over the entire, wild-type sequences; a ClustalW comparison (submitted with the Prior Amendment) of SEQ ID NO:23 with SEQ ID NO:2 of Peak reveals only about 86% identity over the entire, wild-type sequences; and a ClustalW comparison (submitted with the Prior Amendment) of SEQ ID NO:35 with SEQ ID NO:2 of Peak reveals only 77% identity over the entire, wild-type sequences.

In view of the data presented with the enclosures to the Prior Amendment, Applicants cannot understand how the higher level of identity with Masignani or Peak is arrived at by the Examiner.

Further, amended claim 61, reciting that the isolated protein is not a wild-type NhhA protein, and new claim 62, reciting that the isolated protein is a deletion mutant of a wild-type NhhA polypeptide, both are distinguishable over Masignani and Peak. The basis for the anticipation rejections is that sub-regions of the corresponding Masignani and Peak sequences share greater than 90% identity with Applicants' SEQ ID NOS:23 and 35. However, Peak and Masignani do not disclose an isolated protein having at least 90% identity to SEQ ID NOS:23 and 35. Instead, Peak and Masignani disclose a fragment or sub-region of an isolated protein which was not identified explicitly in Peak or in Masignani. The proteins in Masignani and Peak cited by the Examiner are wild-type NhhA proteins. It is only by way of hindsight that the

Examiner has found and artificially extracted the corresponding regions from Peak and Masignani. Thus, claim 61, which excludes wild-type NhhA proteins, does not read on and is not anticipated by the cited references.

Moreover, regarding claim 62, neither SEQ ID NO:4 of Masignani nor SEQ ID NO:21 of Peak is a deletion mutant, and neither Masignani nor Peak discloses or otherwise refers to a deletion mutant. As noted above, the sub-regions identified by the Examiner are from the wild-type proteins in Masignani and Peak.. Thus, claim 62 does not read on and is not anticipated by the cited references.

In view of the significant distinctions between the invention claimed in claims 61 and 62, and the subject matter disclosed in Masignani and Peak, Applicants respectfully submit that the anticipation rejections are moot. Reconsideration and withdrawal of these anticipation rejections are respectfully requested. Moreover, the cited prior art would not render the subject matter of these claims obvious.

Applicants respectfully submit that the present application is now in full condition for allowance and an early Notice of Allowance of all pending claims is respectfully solicited.

Respectfully submitted,

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